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FIGURE 138

MSPPLLKLGAVLSTMAMISNWMSQTLPSLVGLNTRLTSTPDTLTQISPKEGWQVYSSAQDPDG
RCICTVVAPEQNLCSRDAKSRQLRQLLEKVQNMSQSIEVLNLRRTQRDFQYVLKMETQMKGLKA
KFRQIEDDRKTLMTKHFQELKEKMDSELLPLIPVLEQYKTDAKLITQFKEEIRNLSAVLTG IQE
EIGAYDYEELHQRVLSLETRLRDCMKKLTGKLMKITGPVTVKTSGTRFGAWMTDPLASEKNN
RVWYMDSYTNKIVREYKSIADFVSGAESRTYNLPFKWAGTNHVYNGSLYFNKYQSNIIKY
SFDMGRVLAQRSLEYAGFHNVPYTWGGFSDIDLMADEIGLWAVYATNQNAGNIVISQLNQDT
LEVMSWSWSTGYPKRSAGESFMICGTLVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI
SMLDYNARDRALYAWNNGHQVLEFNVTLFHI IKTEDDT

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 215-219

Tyrosine kinase phosphorylation site.

amino acids 106-114

N-myristoylation sites.

amino acids 9-15, 31-37, 235-241, 239-245

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FIGURE 139

GAAGCAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGCTGAGCAAAGGCCTTCACCA**ATG**GCCG
AGTCCCCCGGCTGCTGCTCCGTCTGGGCGGCTGCCTCCACTGCCTGTATAGCTGCCACTGGA
GGAAATGCCCCAGAGAGAGGATGCAAACCAGCAAGTGCGACTGTATCTGGTTTGGCCTGCTCT
TCCTCACCTTCCTCCTTTCCCTGAGCTGGCTGTACATCGGGCTCGTCCTTCTCAATGACCTGC
ACAACCTCAATGAATTCCTCTTCGCGGCTGGGGACACTGGATGGACTGGTCCCTGGCATTCC
TGCTGGTCATCTCTCTACTGGTCACATATGCATCCTTGCTATTGGTCCTGGCCCTGCTCCTGC
GGCTTTGTAGACAGCCCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCTCCTCATTATGC
TGCTTGTGGCGGCTGGCCTTGTGGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC
GTGTGTCACTGCAGGCCACAGCCCCATTCTTCATATTGGAGCAGCCGCTGGAATPGCCCTCC
TGGCCTGGCCTGTGGCTGATACCTTCTACCGTATCCACCGAAGAGGTCCCAAGATTCTGCTAC
TGCTCCTATTTTTTGGAGTTGTCCTGGTCATCTACTTGGCCCCCTATGCATCTCCTCACCT
GCATCATGGAACCCAGAGACTTACCACCCAAGCCTGGGCTGGTGGGACACCGAGGGGCCCCCA
TGCTGGCTCCCGAGAACACCCTGATGTCCTTGCGGAAGACAGCTGAATGCGGAGCTACTGTGT
TTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCTTCCTCATGCATGATGAGCACCTCA
GCAGGACCACGAATGTAGCCTCTGTATTCCCAACCCGAATCACAGCCCACAGCAGTGAATTCT
CCTGGACTGAACTGAAGAGACTCAATGCTGGATCCTGGTTCCCTAGAGAGGCGACCCTTCTGGG
GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAG
AAGAGCTATTGGAGGAAGCTGCAGCCCTCAACCTTTCCATCATGTTGCACTTGCGCCGACCCC
CACAGAACCACACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA
GGGTGCCCCAAGCCATGGTCTTTTGGCTACCAGATGAAGATCGGGCTAATGTCCAACGACGGG
CACCTGGAATGCGCCAGATATATGGACGTCAGGGAGGCAACAGAACGGAGAGGCCCCAGTTTC
TTAACCTCCCCTATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT
CGGTGAACCTATTTGTAGTGAACAAGCCCTGGCTCTTCTCTCTGCTTTGGTGTGCAGGGGTGG
ATTCGGTCACCACCAACGACTGCCAGCTGCTGCAGCAGATGCGTTACCCTATCTGGCTTATTA
CCCCTCAAACCTACCTAATCATATGGGTCATTACCAATTGTGTTTCCACCATGCTGCTTTTGT
GGACCTTCCTCCTCCAAAGGAGATTTGTTAAGAAGAGAGGGGAAACTGGCTTAGAAACAGCAG
TGCTGCTGACAAGGATCAACAATTTTCATGATGGAG**TGA**ATGCCCTGCCCTGCTTCCCCACCCA
AGCCAGTCTACATTGCCCAAACAGCAAGGGTTGGAGAGTGGCTTAAGTGGAATGCTTCAGGGG
TGGTGGGTGCAAGTGGGGGGAGCTTTGCCAACAGGAGGTTTTGAACCATGAGGGCCCTCTGC
CCAGGTGATGGGCATTCCCTAAGCTGCTATGGAATCTGCTCCCTTTGGGGTTTTGACCTGAGA
TGTTTGGGAAGAGAGTGAGTAATGAGAAGTTTCTCCTCAAATGAACTAGAACAGAGGAAGTA
AAAGGGAGATTGCTCGGA

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FIGURE 140

MAESPGCCSVWARCLHCLYSCHWRKCFRERMQTSKDCIWFGLLELTFLLSLSWLYIGLVLLN
DLHNFNEFLFRRWGHWMDSLAFLLVISLLVTYASLLLVLALLLRQLCRQPLHLHSLHKVLLLL
IMLLVAAGLVGLDIQWQQEWHSLRVSLQATAPFLHIGAAAGIALLAWPVADTFYRIHRRGPKI
LLLLLFFGVVLVIYLAPLCISSPCIMEPRDLFPKPGLVGHRGAPMLAPENTLMSLRKTAECGA
TVFETDVMVSSDGVPFLMHDEHLSRTTNVASVFPTRITAHSSDFSWEKRLNAGSWFLERRP
FWGAKPLAGPDQKEAESQTVPALEELLEEAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVL
NARVPQAMVFWLPDEDRAVQRRAPGMRQIYGRQGGRNTERPQFLNLPYQDLPLLDIKALHKD
NVSVNLFVVNKPWLFSLWCAGVDSVTTNDCQLLQQMRYPIWLITPQTYLIWVITNCVSTML
LLWTFLLQRRFVKKRGKTGLETAVLLTRINNEMME

Important features of the protein:**Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506

N-glycosylation sites.

amino acids 349-353, 362-366, 415-419, 442-446

N-myristoylation sites.

amino acids 163-169, 413-419, 523-529

Leucine zipper pattern.

amino acids 93-115, 109-131

Glutamine amidotransferases class-II active site.

amino acids 1-13

FIGURE 141

GCGCGCGGCCCCGGGCTGGAGCCGAGCGCAGCAGCCACCGCCGCCGCCGCCAGAAAGTTTGGGTTGAACCGGAGC
TGCCGGGGAGGAAACTTTTTTCTTTTTTCCCCCTCCCTCCCGGGAGGAGGAGGAGGAGGAGGAGGGGAAGCTGCCG
CCGGCGCCCAAGGCTCGTGGGCTCGGGGTGGCGCGCGCCCGCAGAAGGGGCGGGGGCCTCGCCCGCGAGGGGAGG
CGCGCCCCCGGGGGCCCGAGAGGGGGCGGTGAGGACCGCGGGCTGCTGGTGCGGGCGGGGGCGGCGCGTGTGCCCG
CGCAGGGGAGGGCGCCCCGCCCGCTCCCGGCCCGGCTGCGAGGAGGAGGCGGCGGGCGGCGCAGGAGGATGTACTT
GCTGGCGGGGACAGGGGGTGGCGGGCTGCGGGCACCTCCTGGTCTCGCTGCTGGGGCTGCTGCTGCTGCTGGC
GCGCTCCGGCACCCGGGCGCTGGTCTGCCCTGCCCTGTGACGAGTCCAAGTGCAGGAGGCCAGGAAGTGCCTCGG
GAGCATCGTGACAGGGCGCTCGCGGCTGCTGCTACACGTGCGGCCAGCCAGAGGAACGAGAGCTCGGCGCGGCACCT
CGGGAAATTACGGAACCTGCGACCGGGGGCTGCGTTGTGTCTATCCGCCCCCGCTCAATGGCGACTCCCTCACCG
GTACGAAGCGGGCGTTTGCGAAGATGAGAACGTGGACTGATGACCAACTGCTTGGTTTAAACCATGCAATGAAAA
CCTTATTGCTGGCTGCAATATAATCAATGGGAAATGTGAATGTAAACACCATTCGAACCTGCAGCAATCCCTTTGA
GTTTCCAAGTCAGGATATGTGCCCTTTCAGCTTTAAAGAGAATTGAAGAAGAGAAGCCAGATTGCTCCAAGGCCCG
CTGTGAAGTCCAGTTCTCTCCACGTTGTCTGAAGATTCTGTTCTGATCGAGGGTTATGCTCTCTGGGGAGTG
CTGTCCCTTACCCAGCGCGCTGCGTGTGCAACCCCGCAGGCTGTCTGCGCAAAGTCTGCCAGCCGGGAAACCTGAA
CATACTAGTGTCAAAGCCTCAGGGAAGCCGGGAGAGTGTCTGTGACCTCTATGAGTGCAAACCAAGTTTTCGGCGT
GGACTGCAGGACTGTGGAATGCCCTCCTGTTTCAGCAGACCGCGTGTCCCCCGGACAGCTATGAAACTCAAGTCAG
ACTAACTGCAGATGGTTGCTGTACTTTTGCCAAACAAGATGCGAGTGTCTCTCTGGCTTATGTGGTTTCCCCGTGTG
TGAGGTGGGATCCACTCCCCCGCATAGTCTCTCGTGGCGATGGGACACCTGGAAGAGTGTCTGTATGTCTTTGAATG
TGTTAATGATACAAAGCCAGCCTGGTATTTAAACAATGTGGAATATATGATGGAGACATGTTTGAATGGAACAA
CTGTGCGTTCTGTGATGCCAAGGGGGCTTGGCAATCTGCTCTACTGCGCCAGTGTGGTGAGATAAACTGCGAGAG
GTACTACGTGCCCGAAGGAGAGTGTGCCCCAGTGTGTGAAGATCCAGTGTATCCTTTTAAATAATCCCGCTGGCTG
CTATGCCAATGGCTGTATCCTTGCCACCGGAGACCGGTGGCGGGAAGACGACTGCACATTCTGCCAGTGGCTCAA
CGGTGAACGCCACTGCGTTGCGACCGTCTGCGGACAGACCTGCACAAACCTGTGAAAGTGCCTGGGGAGTGTG
CCCTGTGTGCGAAGAACCAACCATCATCACAGTTGATCCACCTGCATGTGGGGAGTTATCAAACCTGCACTCTGAC
AGGGAAGGACTGCATTAAATGGTTTCAAACGCGATCACAAATGGTTGTGCGACCTGTCAAGTGCATAAACACCGAGGA
ACTATGTTCAGAAGCTAAACAAGGCTGCACCTTGAACCTGTCCCTTCGGTTTCTTACTGATGCCCAAACCTGTGA
GATCTGTGAGTGCCGCCCCAAGGCCCAAGAAGTGCAGACCAATAATCTGTGACAAGTATGTCCACTTGGATTGCT
GAAGAATAAGCACCGCTGTGACATCTGTGCTGTGAAGAAATGTCCAGAGCTCTCATGACGTAAGATCTGCCCTT
GGGTTTCCAGCAGGACAGTCAACGGCTGTCTTATCTGCAAGTGCAGAGAGGCTCTGCTTCACTGGGGCCACCCAT
CCTGTGCGGGCACTTGTCTCACCGTGGATGGTCTCATCATATAAAATGAGGAGAGCTGGCACGATGGGTGCCGGGA
ATGCTACTGTCTCAATGGACGGGAAATGTGTGCCCTGATCACCTGCCCGGTGCCCTGCCCTGTGGCAACCCACCAT
TCACCTTGGACAGTGTCTGCCCATCATGTGCAGATGACTTTGTGGTGCAGAAGCCAGAGCTCAGTACTCCCTCCAT
TTGCCACGCCCTTGGAGGAGAATACTTTGTGGAAGGAGAAACGTGGAACAATTGACTCCTGTACTCAGTGCACCTG
CCACAGCGGACGGGTGCTGTGTGAGACAGAGGTGTGCCACCGCTGCTCTGCCAGAACCCCTCACGCACCCAGGA
TTCTGCTGCCACAGTGTACAGATCAACCTTTTCGGCTTCTCTGTCCCGCAATAACAGCGTACCTAATTAAGT
CAAAAATGATGAAGGGGATATATTCCTGGCAGCTGAGTCTTGAAGCCTGACGTTTGTACAGCTGCATCTGCAT
TGATAGCGTAATAGCTGTCTCTGAGTCTCTGCCCTCTCTGATCCTGTGAAAGACCTGTCTTGAGAAAGGCCA
GTGTTGGTCCCTACTGCATAGAAGACAAATTCCAAAGAAGTGGTGTGCCACTTCAGTGGGAAGGCCATTGCGGA
CGAGGAGCGGTGGGACCTTGACAGCTGCACCCACTGCTACTGCCCTGCAGGGCCAGACCCCTCTGCTCGACCGTCA
CTGCCCCCTCTGCCCTGTGTTGAGCCCATCAACGTGGAAGGAAGTTGCTGCCCAATGTGTCCAGAAATGTATGT
CCCAGAAACCAACCAATATACCCATTGAGAAGACAAACCATCGAGGAGAGGTTGACCTGGAGGTTCCCCGTGTGGC
CACGCTTAGTGAAAATGATATCGTCCATCTCCCTAGAGATATGGGTACCTCCAGGTAGATTACAGAGATAACAG
GCTGCACCCCAAGTGAAGATTCTTCACTGGACTCCATTGCCCTCAGTTGTGGTTCCCATATAATTATATGCCCTCTCTAT
TATAATAGCATTCCTATTTCATCAATCAGAAGAAACAGTGGATACCCTGCTTTGCTGGTATCGAACACCAACTAA
GCCTTCTTCTTAAATAATCAGCTAGTATCTGTGGACTGCAAGAAAGGAACAGAGTCCAGGTGGACAGTTCOCA
GAGAATGCTAAGAATTGCAGAACCAGATGCAAGATTCACTGGCTTCTACAGCATGCAAAAAACAGAACCTTACA
GGCAGACAAATTTATACCAACAGTGTGAAGAAAGGCAACTAGGATGAGGTTTCAAAAGACGGAAGACGACTAAAT
CTGCTCTATAAAAGTAAACATAGAAATTTGTGCACCTGTCTTAGTGGATTGTATTTGGATTGTGACTTGTATGACAGCGC
TAAGACCTTACTGGGATGGGCTCTGTCTACAGCAATGTGCAGAACAGCAATTCACCTTTTCTCAAAAAA

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FIGURE 142

MYLVAGDRGLAGCGHLLVSLGLLLLLLARSCTRALVCLPCDESKCEEPRNCPGSIVQGVCGCC
 YTCASQRNESCGGTFGIYGTCDRGLRCVIRPPLNGDSLTEYEAGVCEDENWTDQLLGFKPCN
 ENLIAGCNIIINGKCECNTIRTCNPFEEFPSQDMCLSALKRIEEEEKPDCSKARCEVQFSFRCPE
 DSVLIEGYAPPGECCPLPSRCVCNPNAGCLRKVCQPGNLNILVSKASGKPGGCCDLYECKPVFG
 VDCRTVECPVQQTACPPDSYETQVRLTADGCCTLPTRCECLSGLCGFPVCEVGSTPRIVSRG
 DGTPGKCCDVFEVCVNDTKPACVFNNVEYYDGMFRMDNCRFCRCQGGVAICFTAQCCEINCR
 YYVPEGECCPVCEDPVYFPFNNPAGCYANGLILAHGDRWREDDCTFCQCVNGERHCVATVCGQT
 CTNPVKVPGECCPVCEEPTIITVDPPACGELSNCTLTGKDCINGFKRDHNGCRTQCQCINTEEL
 CSERKQGCTLNCPPFGFLTDAQNCEICECRPRPKKCRPIICDKYCPLGLLKNKHGCDICRCKKC
 PELSCSKICPLGFQQDSHGCLICKCREASASAGPFILSGTCLTVDGHHHKNEESWHDGCRECY
 CLNGREMCALITCPVPACGNPTIHPGQCCPSCADDFVQKPELSTPSICHAPGGGEYFVEGETW
 NIDSCTQCTCHSGRVLCETEVCPPLLQNPSTQDSCCPQCTDQFFRPSLSRNNSVFNYCKND
 EGDIFLAESWKPDVCTSCICIDSVISCFSESCPSVSCERPVLKRGQCCPYCIEDTIPKKVVC
 HFSGKAYADEERWDLDSCTHCYCLQGQTLCTVSCPPLPCVEPINVEGSCCPMCPPEMYVPEPT
 NIPIEKTNHRGEVDLEVPLWPTPSENDIVHLPRDMGHLQVDYRDNRHLHPSEDSSLDIASVVV
 PIIICLSIIIAFLFINQKKQWIPLLCWYRTPTKPSLNNQLVSVDCCKGTRVQVDSSQRMRLRI
 AEPDARFSGFYSMQKQNHLOADNFYQTV

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 940-962

N-glycosylation sites.

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 992-996

N-myristoylation site.

amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,
 439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,
 845-851

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 52-63, 844-855

Cell attachment sequence.

amino acids 314-317

Leucine zipper pattern.

amino acids 3-25

Eukaryotic thiol (cysteine) proteases cysteine active site.

amino acids 57-69

VWFC domain proteins.

amino acids 448-456, 382-390

C-terminal cystine knot proteins

amino acids 60-86

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FIGURE 143

GACGTCTGGCCGGCTCCCGGCGAAGGGCAGCGGAGGAGCGGCCCCAGAGCGCGCAGCTAGGGCA
CTGGCGAAACCCCGGGACAGTCCCTCTCCGTGCGGGGGCGGCGCAGAGCAGTCCCATCCCCG
GGTCCCGGGCGCGGCTGACTGCCGGCTGGTTCCCTGCGCGCAGTAGCTCCCCGAGCCGGGCTG
CACCGGAGGCGGCGAGATGGTGCGCGCGCTCGGCCTCCTGCTGCGCGCCCTGCAGCTGCTACT
GTGGGGGCCACCTGGACGCCAGCCCGCGGAGCGCGGAGGCCAGGAGCTGCGCAAGGAGGCGGA
GGCATTCCTAGAGAAGTACGGATACCTCAATGAACAGGTCCCCAAAGCTCCACCTCCACTCG
ATTCAGCGATGCCATCAGAGCGTTTCAGTGGGTGTCCAGCTACCTGTCAGCGGCGTGTTGGA
CCGCGCCACCCTGCGCCAGATGACTCGTCCCCGCTGCGGGGTACAGATACCAACAGTTATGC
GGCCTGGGCTGAGAGGATCAGTGACTTGTTTGCTAGACACCGGACCAAAATGAGGCGTAAGAA
ACGCTTTGCAAAGCAAGGTAACAAATGGTACAAGCAGCACCTCTCCTACCGCCTGGTGAAGT
GCCTGAGCATCTGCCGGAGCCGGCAGTTCGGGGCGCCGTGCGCGCCGCCTTCCAGTTGTGGAG
CAACGTCTCAGCGCTGGAGTTCTGGGAGGCCCCAGCCACAGGCCCCCGCTGACATCCGGCTCAC
CTTCTTCCAAGGGGACCACAACGATGGGCTGGGCAATGCCTTTGATGGCCCAGGGGGCGCCCT
GGCGCACGCCTTCCTGCCCCGCGCGGCGGAAGCGCACTTCGACCAAGATGAGCGCTGGTCCCT
GAGCCGCCCGCCGCGGGCGCAACCTGTTTCGTGGTGTGGCGCACGAGATCGGTCACACGCTTGG
CCTCACCCACTCGCCCGCGCCGCGCGCTCATGGCGCCCTACTACAAGAGGCTGGGCCGCGA
CGCGCTGCTCAGCTGGGACGACGTGCTGGCCGTGCAGAGCCTGTATGGGAAGCCCCCTAGGGG
CTCAGTGGCCGTCCAGCTCCCAGGAAAGCTGTTCACTGACTTTGAGACCTGGGACTCCTACAG
CCCCAAGGAAGGCGCCCTGAAACGCAGGGCCCTAAATACTGCCACTCTTCCTTCGATGCCAT
CACTGTAGACAGGCAACAGCAACTGTACATTTTTTAAAGGGAGCCATTTCTGGGAGGTGGCAGC
TGATGGCAACGTCTCAGAGCCCCGTCCACTGCAGGAAAGATGGGTCCGGCTGCCCCCAACAT
TGAGGCTGCGGCAGTGTCATTGAATGATGGAGATTTCTACTTCTTCAAAGGGGGTGCATGCTG
GAGGTTCCGGGGCCCCAAGCCAGTGTGGGGTCTCCACAGCTGTGCCGGGCAGGGGGCCTGCC
CCGCCATCCTGACGCCGCCCTCTTCTTCCCTCCTCTGCGCCGCCTCATCCTCTTCAAGGGTGC
CCGCTACTACGTGCTGGCCCGAGGGGGACTGCAAGTGGAGCCCTACTACCCCCGAAGTCTGCA
GGACTGGGGAGGCATCCCTGAGGAGGTGAGCGGCGCCCTGCCGAGGCCCGATGGCTCCATCAT
CTTCTTCCGAGATGACCGCTACTGGCGCCTCGACCAGGCCAACTGCAGGCAACCACCTCGGG
CCGCTGGGCCACCGAGCTGCCCTGGATGGGCTGCTGGCATGCCAACTCGGGGAGCGCCCTGTT
CTGAAGGCACCTCCTCACCTCAGAACTGGTGGTGCTCTCAGGGCAAAATCATGTTCCCCACC
CCCGGGGCAGAACCCCTCTTAGAAGCCTCTGAGTCCCTCTGCAGAAGACCGGGCAGCAAAGCC
TCCATCTGGAAGTCTGTCTGCCTTTGTTCTTGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 144

MVARVGLLLRALQLLLWGHLDQAQPAERGGQELRKEAEAFLEKYGYLNEQVPKAPTSTRESDAI
RAFQWVSQLPVSGVLDRATLRQMTRPRCGVTD'TNSYAAWAERISDLFARHRTKMRRKKRFAKQ
GNKWKQHLSTYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD
HNDGLGNAFDGPGGALAHAFLLPRRGEAHFDQDERWSLSRRRGRNLFVFLAHEIGHTLGLTHSP
APRALMAPYYKRLGRDALLSWDDVLAVQSPLYGKPLGGSVAVQLPGKLFTDFETWDSYSPQGRR
PETQGPKYCHSSFDAITVDRQQQLYIFKGSHEWEVAADGNVSEPRPLQERWVGLPPNIEAAAV
SLNDGDFYFFKGGRCWRFRGPKPVWGLPQLCRAGGLPRHPDAALFFPPLRRLILFKGARYYVL
ARGGLQVEPYYPRLQDWGGIPEEVSGALPRPDGSIIFRRDDRYWRLDQAKLQATTSGRWATE
LPWMGCWHANSGSALF

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 355-359

N-myristoylation sites.amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,
509-515**Amidation site.**

amino acids 312-316

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 237-247

Matrixins cysteine switch

amino acids 231-262, 271-284

Hemopexin domain protein

amino acids 66-108, 231-262

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FIGURE 145

GCCGGCTAGGGCGCCGGAGCCGCACGCAGCCGCGGGGCTCCGAGAGGGCGCGCACTGGGGCTGGGACTGCGCGGCG
CCGCCGCTGCGAGCGCCACTGAGCGGTGCGGCAACTTCGGAGGCACAGCGCCGGAGCCAGGCGAGCGCTCAGAGA
CCCGGAGCCAGAGGGGCGCGCCGGAGCCTCGTTGAGAGCCGGCGCCAGGCACCCACCGCGCTCCGAGTGCCAGG
CGGCCCTCCGCGCAGCGTGCTTCCGCTGCCCCACGGAAGGCACGGGCTGGCGCTGCCGGGCGCCGGGGAGGAC
GGCGAGGAGGAGGCGGCGGGCGGAGACGGCGGCGGCGAGACTGGGGCCAGGGAGACAGCCCTGGGGGAGAGGC
GCCCCAACCAGGCCGCGGGAGCATGGGGGGCCCGGAGCGGAGCTCGGGGCGCGCTGCTGCTGGCACTGCTGCTCTG
CTGGGACCCGAGGCTGAGCCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCCTGACTCCTTCCCCTCAGCGCC
AGCAGAGCCGCTGCCCTACTTCTTGCAGGAGCCACAGGACGCTACATTGTGAAGAACAGCCTGTGGAGCTCCG
CTGCCGCGCCTTCCCCGCCACACAGATCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACACGTAC
ACAGGAAGGCCTGGATGAGGCCACCGGCCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTGCGGGCAGCAGGTGGA
GGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAGGCACACCACAGAGTCGCCG
AGCCTACGTCCGCATCGCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCA
TGAGGTTCTCTGCACTGCCGCCCGCGGAGGGGGTGCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGT
CATCGACCCACCCAGGACACCAACTTCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCCTGTC
GGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGCCCAAACGCCGGAGCACCACTGCCACCGTCACTGT
CTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCACCCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAA
GCGCACCCGGACCTGCACCAACCCCGCTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGAC
CGCTGCAACCACTCTGCCAGTGCATGGGGGCTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTGAGTG
TGCCCACTGGCGTAGCCGCGAGTGATGGCGCCCCACCCAGAACGGAGGCGGTGACTGCAGCGGGACGCTGCT
CGACTCTAAGAAGTGCACAGATGGGCTGTGCATGCAAAATAAGAAAATCTAAGCGACCCACAGCCACCTGCT
GGAGGCTCAGGGGATGCGGCGCTGTATGCGGGCTCGTGGTGCCATCTTCGTGGTCTGGCAATCCTCATGGC
GGTGGGGGTGGTGGTGTACCGCCCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGAC
TGGTGGTTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGCAACCCGACGCTCCTACACCCCTCTGTGCCTCC
TGACCTGACAGCCAGCGCCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCAT
GACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGG
GCCAGGCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCTGGCACATACCTAGCGATTTCGCCCGGGA
CACCACCTTCTGCACTGCGCAGCGCCAGCCTCGGTTCCCGAGAGCTCTTGGGCTGCCCGAGACCCAGGGAG
CAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGTGGTGCC
CAATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTCCCGCT
TTCAGAAGGGACCCAGACAGTATTGAGCCCCCTCGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCGCT
CATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGAAGTCTTTCAGCTCAAGACCCAGGCCACCA
GGGCCACTGGGAGGAGGTGGTGACCTGGATGAGGAGACCTGAACACACCCCTGCTACTGCCAGCTGGAGCCAG
GGCCTGTACATCCTGCTGGACAGCTGGGCACCTACGTGTTACGCGGCGAGTCTTATCCCCTCAGCAGTCAA
GCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCCTGGA
GGACACGCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAA
ACCGTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCATGCCATTGGAGGAG
CAGCTGCTGGCCAAATACCAGGAGATCCCCCTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCAC
TTTCACCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAGTGGAGGGGA
GGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCC
TGGCAGCACTGTACACCCAGCTGGGACCTTATGCCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAA
CAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCT
GAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGG
GGACCTCAACAGCCTGGCGAGTGCCCTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGG
GGACTGCTAGCCCTCCTGGGACAGCGGGCTGCCAGGAGTGGCAGGAGGCAGGTGCAGGGAGGCTGGGGCAGCC
TCCTGATGGGGATGTTTGGCCTCTGCTTCTCCAGTTTACAGCCAGAGTTGCCCTCTCCTCCTCCTCTCCCCAA
CCCCAGACCATGACCAGCCTTAGAAAATCCATGTAATCTGTTGTTAGAGGGCCAGAGTTTCTTCTCCACCCCC
GCTCTCTCTCTTGGCCTGAGATCTCTGTGCAGGAACCAAGATGGGGCTGAGGCCTCTGGAGGCAGTTGGTTGG
GGGCGGGCAGGCAGGAGGCCCTCCCTCCACCCCCCCCCACCTCAGCCCCGCAACTTCTGGGTTCGGTGGGTTTTAG
TTCCGTTCTTCTTTTCTTCTCCGTTATGATTTCTCCTTTCTCCCTAAGCCCCCTTCTGCTTCCACGCCCTTT
TCCTCTTTGAAGAGTCAAGTACAATTACAGACAACTGCTTTCTCCTGTCCAAAAGCAAAAAGGCAAAAGGAAAGAA
AGAAAGCTTCAGACCGCTAGTAAGGCTCAAAGAAGAAGAAAAACACCAAAACCACAAGGGAAGAAAGAAACCCAG
TTCTTAGGAAACGCAACGATTTATTATCCAGATTATTTGGATAAGTCTTTTAAAA

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FIGURE 146

MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIVKNK
 PVELRCRAFPATQIYFKNGEWSQNDHVTQEGLEATGLRVREVQIEVSRQQVEELFGLEDY
 WCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGVPVAEVEWLK
 NEDVIDPTQDTNFLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW
 AEWSPCSNRCGRGWQKRTRCTNPAPLNGGAFCEGQAFQKTACTTICPVDGAWTEWSKWSACS
 TECAHWSRRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKTLSDPNSHLLEASGDAALYA
 GLVVAIFVVVAILMAVGVVVYRRNCRDFTDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV
 PPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLPSLKVKVYSSSTTGSGPGLADGADLLG
 VLPPGTYPSTDFARDTHFLHLRSASLGSQLGLPRDPGSSVSGTFGCLGGRLSIPGTGVSLLV
 PNGAIPQKGKPYEMYLLINKAESTLPLSEGTQTVLSPSVTCGPTGLLLCRPVILTMPHCAEVSA
 RDWIFQLKTOAHQGHWEVVTLDEETLNTPCYQCLEPRACHILLDQLGTYVFTGESYSRSAVK
 RLQLAVFAPALCTSLEYSRLVYCLEDTPVALKEVLELERTLGGYLVVEPKPLMFKDSYHNRL
 SLHDLPHAHWSKLLAKYQEIPFYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEG
 QIFQLHTTLAETPAGSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDRM
 LAQKLSMDRYLNYFATKASPTGVILDLWEALQQDDGDLNSLASALEEMGKSEMLVAVATDGDC

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 374-395

N-glycosylation sites.

amino acids 222-225, 347-350

Glycosaminoglycan attachment site.

amino acids 492-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 233-236, 234-237

Casein kinase II phosphorylation sites.

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

Tyrosine kinase phosphorylation sites.

amino acids 216-223, 773-780

N-myristoylation sites.

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 541-551

ATP/GTP-binding site motif A (P-loop).

amino acids 926-933

Growth factor and cytokines receptors family signature 2.

amino acids 306-312

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FIGURE 147

GAGAGGGACAGAGGCTGGAGAAGGATGTATGGCCTGCCCTGGGCTTGTCTGTTCCCTCCTGAGCCTGAGCCCCTT
ACCTTCCTGACCCCATGAAGCACACACTGGCTCTGCTGGCTCCCTGCTGGGCCTGGGCCTGGGGCTGGCCCTGA
GTCAGCTGGCTGCAGGGGCCACAGACTGCAAGTTCTTGGCCCCGAGAGCACCTGACATTCACCCAGCAGCCA
GGGCCCCGGTGGCTGGCCCCCTCGAGTTCTGTCGCCAGGACTCCTGGACTCCCTCTATGGCACCGTGCGCCGCTTCC
TCTCGGTGGTGCAGCTCAATCCTTTCCCTTCAGAGTTGGTAAAGGCCCTACTGAATGAGCTGGCCCTCCGTGAAGG
TGAATGAGGTGGTGCAGTACGAGGCGGGCTACGTGGTATGCGCTGTGATCGCGGGCTCTACCTGCTGCTGGTGC
CCACTGCCGGGCTTTGCTTCTGCTGCTGCCGCTGCCACCGGCGCTGCGGGGGACGAGTGAAGACAGAGCACAAGG
CGCTGGCCTGTGAGCGCGCGGCCCTCATGGTCTTCTGCTGCTGACCACCTCTGCTGCTGATTGGTGTGGTCT
GTGCCTTTGTACCAACACAGCGCACCGCATGAACAGATGGGCCCCAGCATCGAGGCCATGCCCTGAGACCTGCTCA
GCCCTGCGGGCTGGTCTCTGATGTCCCCAAGAGCTGCAGGCCGTGGCACAGCAATTCTCCCTGCCCGAGGAGC
AAGTCTCAGAGGAGCTGGATGGTGTGGTGTGAGCATTGGGAGCGCGATCCACACTCAGCTCAGGAGCTCCGTGT
ACCCCTTGTCTGGCGGCCGTGGGCAGTTTGGGCCAGGTCTGCGAGGTCTCCGTGCACCACCTGCAAACCTTGAATG
CTACAGTGGTAGAGCTGCAGGGCGGGCAGCAGGACCTGGAGCCAGCCATCCGGGAACACCGGGACCGCCTCCTTG
AGCTGCTGCAGGAGGCCAGGTGCCAGGGAGATTGTGCAGGGGCCCTGAGCTGGGCCCCGACCTGGAGCTGGGTG
CTGACTTCAGCCAGGTGCCCTCTGTGGACCATGTCTGCAACAGCTAAAAGGTGTCCCCGAGGCCAACTTCTCCA
GCATGGTCCAGGAGGAGAACAGCACCTTCAACGCCCTTCCAGCCCTGGCTGCCATGCAGACATCCAGCGTGGTGC
AAGAGCTGAAGAAGGCAGTGGCCCAGCAGCCGGAAGGGGTGAGGACACTGGCTGAAGGGTTCCCGGGCTTGGAGG
CAGCTTCCCGCTGGGCCCAGGCACTGCAGGAGGTGGAGGAGAGCAGCCGCCCTACCTGCAGGAGGTGCAGAGAT
ACGAGACCTACAGGTGGATCGTGGGCTGGCTGCTGCTGCTCCGTGGTCCATATTGCTGGTGTCTGCAACCTGCTGG
GCCTCAATCTGGGCATCTGGGGCTGTCTGCCAGGGACGACCCAGCCACCCAGAAGCCAAAGGCGAGGCTGGAG
CCCGCTTCTCATGGCAGGTGTGGGCCTCAGCTTCTCTTTGCTGCACCCCTCATCCTCCTGGTGTTCGCCACCT
TCCTGGTGGGTGGCAACGTGCAGACGCTGGTGTGCCGGAGCTGGGAGAACGGCGAGCTCTTTGAGTTTGCAGACA
CCCCAGGGAACCTGCCCCCGTCCATGAACCTGTCCGAACCTTCTTGGCCTGAGGAAGAACATCAGCATCCACCAAG
CCTATCAGCAGTGAAGGAAGGGGAGCGCTCTGGACAGTCTGCAAGCTCAACGACTCTTACGACCTGGAGGAGC
ACCTGGATATCAACAGTATACCAACAAGCTACGGCAGGAGTTGCAGAGCCTGAAAGTAGACACACAGAGCCTGG
ACCTGCTGAGCTCAGCCGCCCGCGGGACCTGGAGGCCCTGCAGAGCAGTGGGCTTCAGCGCATCCACTACCCCG
ACTTCTCTCGTTAGATCCAGAGGCCGTGGTGAAGACCAAGCATGGAGCAGCTGGCCCAAGGAGCTGCAAGGACTGG
CCCAGGCCCAAGACAATTCTGTGCTGGGGCAGCGGCTGCAGGAGGAGGCCCAAGGACTCAGAAACCTTACCAGG
AGAAGGTCTCCCCAGCAGAGCCTTGTGGCAAAGCTCAACCTCAGCGCTCAGGGCCCTGGAGTCTCTGCCCGCA
ATCTCCAGCTGGAGACCTCAGATGTCTAGCCAATGTCACTACCTGAAAGGAGAGCTGCCTGCCCTGGGCAGCCA
GGATCCTGAGGAATGTGAGTGAAGTGTTCCTGGCCCCGGAGATGGGCTACTTCTCCAGTACGTGGCCCTGGGTGA
GAGAGGAGGTGACTCAGCGCATTTGCCACCTGCCAGCCCCCTCTCCGGAGCCCTGGACAACAGCCGTGTGATCCTGT
GTGACATGATGGCTGACCCCTGGAATGCCCTTCTGGTCTGCTGGCATGGTGCACCTTCTTCTGATCCCCAGCA
TCATCTTTGCCGTCAAGACCTCCAAATACTTCCGTCTATCCGGAAACGCCCTCAGCTCCACCAGCTCTGAGGAGA
CTCAGCTCTTCCACATCCCCCGGGTTACCTCCCTGAAGCTGTAGGGGCTTGTGGGGTGAAGTGAACCTGAGGCTG
CCTGTCTCCCTTTGATTAGCTTGGGCCACAGGACTTCGGTAGCTCTTGCCCCAGAGCCAGGCTGGCATCCA
GGCTGGACTGTCCCAGTTCCGGCTTACCTGGCCCCACCTTGCTGCTCCTTTCACCCCTTTCTGCTCAGCAC
CCCCATCAFTCAGCTCAGAATCACATGGGACTTCTGTGAGCTGCAGAGCCAGCAAGTCCCTACAGGTGTCAAC
CGTTACCCCCATGCTGGTGGCATCTCACAGGAAGAGCCTGTTCTCCACCTGCTGGAGCCTGGACCCTGGGGTGG
GACAGAGGCTCGTCCAACCCCACTCCCTTCCCGTGTGTCTTCCCCCTGCCAAGCTTCCCCCTGCCAAGCCTCC
CCCTGCCCTCTCTGAGCCCTCGCCCCCACACCGTCTCATCTGGCTCCCCCTGGCCCCCACTTCCCTCTT
ATGCCCTTCTGGCCCTTTGCTTCTCCTCCTTAGTCCCTCTTACCATATCTCCACTGCTACCTTGTGGCCCCA
GAGACCACCTTGCCCAACCAAAACCACTCAGGTAACGCCACTAATCAGGCAGGGGCCACCATGGCCTAGGTCTGGG
CTGGCTGCAGGCCCTGCCTCATGGCTCTGAGCCCTCCACTGCCCCAGGCCCTTGGGCCCTCTGCAGATCTCATC
CAGGATTTATTGTTGTCCAGTGGGTGAGGGAGGCCTGTCTGAAGGCCGAGCCTCCCTGCCTGCACCAAGTTAG
AAATGGGGGTACCAGCACTTAGCTTCTCTCTGAGTGTGGCTCCCAAGGAAGGGACCTGGGACCTGGGCCACAGT
GGGGGCTTGGCCTTACCTCTTCAGAAGGAAGCATCTTCCACAGCCCCCAACCACTTTCTTAGGAGTGATCTGGT
GGCCAGAACAGGATTTTGCACGGCCCCCTTTTATCTGCGCATGTGGCCTAGGGTCACTCCCGAGCCCATCCCTGTG
TCAGCCCTGAGTGTGGACACTCGTTCAGAAATGAGGAAGAGGAGAGAGAAGAGATGGACAGACCTCAGATCC
ATTAAAGTGTCTCACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 148

MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL
 DSLYGTVRRFLSVVQLNPFPSSELVKALLNELASVKVNEVVRYEAGYVVCVAVIAGLYLLL
 PTAGLCFCCCRCHRRRCGGRVKTEHKALACERAALMVFLLLTLLLLIGVVCAVFTNQTH
 EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAQQFSLPQEQVSEELDGVGVSIGSAIHTQ
 LRSSVYPLLAAVGSLGQVLQVSVHHLQTLNATVVELQAGQQDLEPAIREHRDRLELLQE
 ARCQGDCAAGALSWARTLELGADFSQVFSVDHVLHQLKGVPEANFSSMVQEEENSTFNALPA
 LAAMQTSSVVQELKKAVAQQPEGVRTLAEGFPGLEAASRWAQALQEEVEESSRPFYLQEVQR
 YETRWIVGCVLCSVVLFFVLCNLLGLNLGIWGLSARDPPSHPEAKGEAGARTLMAGVGL
 SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLLGLRKN
 ISIHQAYQQCKEGAALWTVLQLNDSYDLEEHLDINQYTNKLRQELQSLKVDTSQSLDLLSS
 AARRDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE
 EAQGLRNLHQEKVVPQQSLVAKLNLSVRALESSAPNLQLETSDVLANVTYLGELPAWAA
 RILRNVSECFIAREMGYFSQYVAWVREEVTQRIATCQPLSGALDNSRVILCDMMADPWNA
 FWFCLAWCTFFLIPSIIFAVKTSKYFRPIRKRLSSTSSEETQLFHIPRVTSCLK

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

N-glycosylation sites:amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,
684-688, 707-711, 725-729**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 811-815

Tyrosine kinase phosphorylation site.

amino acids 95-103

N-myristoylation sites.amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,
228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,
477-483, 500-506, 536-542, 644-650, 761-767**Phospholipase A2 histidine active site.**

amino acids 129-137

4Fe-4S ferredoxins, iron-sulfur binding region signature.

amino acids 126-138

Mitochondrial energy transfer proteins signature.

amino acids 80-89

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FIGURE 149

CACAGCTCCCTTCCCAGGACGTGAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCA
GCCTGCTCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTG
CCAAGGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC
TTTGGGTGGTGCCTGGGGCACTCCCACAGGTGTAGCACCTCCCAAAGCAAGACTCCAGACAGCG
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCCTTTCAGCCTTCAC
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGGCTGCAAGGACCCTGGGAAAGTTCCAG
AACTCCACGTCCTTGTCTCAATTGTGCCATCAACTTTCAGAGCTATCATGAGCCAACCTCACC
CCACAGGGCCTCAGTCGCCACCATGTGGGCCTCTCCAGTGCAAACCACCGAGCATTCCACCAT
GACCGGTCACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAAGGTGGCAAGCACC
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTTCAGGTCCATTTCAGCCTCCTGGCA
TTTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTCCTAGCCTCCTGACATGAGTCTGC
TGGAAAGAGCATCCAAACAAACAAGTAATAAATAAATAAATAAACTCA

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FIGURE 150

MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVPSPNSTNLKGHHVRLCKPC
KLEPEPRLWVVP GALPQV

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 48-52

Amidation sites.

amino acids 23-27, 33-37

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FIGURE 151

CACCGGAGGGACGCGAGCTGACGGAGCTGCGCTGCGTTCCGCTCGTTTGCCTCGCGCCCTCCA
CTGGAGCTGTTTCGCGCCTCCCGGCTCCCACCGCAGCCCACCCGGCAGAGGAGTCGCTACCAGC
GCCCAGTGCCTCTGTCTAGTCCGCAAACCTCCTTGCCGCCCCGCCCCGGGCTGGGCACCAAATAC
CAGGCTACCATGGTCTACAAGACTCTCTTCGCTCTTTGCATCTTAAGTGCAGGATGGAGGGTA
CAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCACCGACC
ACCATCTGGACTAGCTCTCCACAAAACACTGATGCAGACACTGCCTCCCCATCCAACGGCACT
CACAACAACCTCGGTGCTCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAAGAACATT
TCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTTGAATTGGGAAGGCACAAACACA
GACCCCTCACCTTCTGGGTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACCACGTTGGAG
GAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTTCGAGTCCGCTGCTGAG
CCTCCACACTCATCTCCCCTCAAGCTCCAGCTCATCACCTCATCCCTATCAACCTCACCA
CCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACCAGCACCCCAACCC
ACTGGAGCTCCAAGTGCACACAGAGTCCCCGACAGAGGAGTCCAGCTCTGACCACACACCCACT
TCACATGCCACAGCTGAGCCAGTGGCCAGGAGAAAACACCCCCAACAACTGTGTTCAGGCAAA
GTGATGTGTGAGCTCATAGACATGGAGACCACCACCACCTTTCCAGGGTGATCATGCAGGAA
GTAGAACATGCATTAAAGTTCAGGCAGCATCGCCGCCATTACCGTGACAGTCATTGCCGTGGTG
CTGCTGGTGTGTTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCCCTCCTATGGAAGACTTTTG
GACGACCATGACTACGGGTCTGGGGAAACTACAACAACCTCTGTACGATGACTCCTTAACAA
TGAATAATGGCCTGGGATGAGGATTAAGTGTCTTTATTTATAAGTGCTTATCCAGTAGAATT
AATAAGTACCTGATGCGCATTGAACGACAATCTTAAGCCCTGTTTTGTTGGTATGGTTGTTTT
TGTTTTCTCTCCCTCTCCTCTGGCTGCTACAACCTTCCCCTTTCTGGTACAAGAAGAACCATTCT
TTAAAGGTGAGTGGAGGCTGATTTCAGCTGAAGTGGGCCAGCCTTGACACAGCCAGGCCAGA
CCACCATGGTGAAGGCTTCTTTCCCCACTGCAGGACCCACTTTGAGAAGGATCGAGGAGGAGG
ATTTGGGTGTTTTGTTAGGGGTTACTTTCAGGGGAACATTTCAATTGTGTATTCTTTAAAC
TTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGAAGGAAATGAGCTCTACGAGGATTT
CACCTTGCTGAGGAGAGAGCAGGGTTTTCTCAGATTCTTTTAAATCTCTATTTATCTGGTTG
TTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGCTGGAAAGCAGCTTCTTAGCTGCCTAAT
TAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGGGGCCAGCAGGTCACGGGGCAGAATCTCT
CAGGTTGCTGTGGGATCTCAGTGTGCCCTACCTGTTCTCCCCTCCAGGCCACCTGTCTCTGT
AAAGGATGCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCACAAGTGATCAGCAGAGTT
GCATTTCCAAAGAAAAGGCTATGAGATGAGCTGAGTTATAGAGAGAAAGGGAGAGGCATGTA
CGGTGTGGGAAGTGGAAGAGAAGCTGGCGGGGGAGAAGGAGGCTAACCTGCACTGAGTACTT
CATTAGGACAAGTGAGAATCAGCTATTGATAATGGCCAGAGATATCCACAGCTTGGAGGAGCC
CAGAGACTGTTTGCTTTATACCCACACAGCAACTGGTCCACTGCTTTACTGTCTGTGGATAA
TGGCTGTAAATGTTTAAAAAC

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FIGURE 152

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNN
SVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEEHS
SGTPEAGVAATLSQSAAEPPTLISQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQOPTGA
PTAPESPTEESSSDHTPTSHATAEPVPQEKTEPPTTVSGKVMCELIDMETTTTFPRVIMQEVEH
ALSSGSIAAITVTVIAVVLLVFGVAAYLKIRHSSYGRLLDDHDYGSWGNYNPNPLYDDS

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 258-278

N-glycosylation sites.

amino acids 58-61, 62-65, 80-83, 176-179

Casein kinase II phosphorylation sites.amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-
144, 164-167, 191-194, 195-198, 200-203**Tyrosine kinase phosphorylation site.**

amino acids 289-296

N-myristoylation sites.

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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FIGURE 153

[illegible]

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FIGURE 154

MLVHCVGLLLTGLLLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV
LGTLLLGSAVLVACVDYFLEGLALGSWLGQRLQTLPALPSLC

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 38-55, 60-78

N-myristoylation sites.

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 67-78

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FIGURE 155

TGCAATTAAAGGAGTCGGGTCTCTAACTGTTGATCTGTTTTTTCCCTTCTGAGCA**ATG**GAGC
TTACCATCTTTATCCTGAGACTGGCCATTTACATCCTGACATTTCCCTTGTACCTGCTGAACT
TTCTGGGCTTGTGGAGCTGGATATGCAAAAATGGTTCCCTACTTCTTGGTGAGGTTCACTG
TGATATACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTCTTCAGTAACCTGCAGGAGTTTG
CGGGCCCCCTCCGGGAAACTCTCCCTGCTGGAAGTGGGCTGTGGCACGGGGGCCAACTTCAAGT
TCTACCCACCTGGGTGCAGGGTGACCTGTATTGACCCCAACCCCAACTTTGAGAAGTTTTTGA
TCAAGAGCATTGCAGAGAACCGACACCTGCAGTTTGAGCGCTTTGTGGTAGCTGCCGGGGAGA
ACATGCACCAGGTGGCTGATGGCTCTGTGGATGTGGTGGTCTGCACCCTGGTGCTGTGCTCTG
TGAAGAACCAGGAGCGGATTCTCCGCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGGCTTTCT
ATTTTCATGGAGCATGTGGCAGCTGAGTGTTCGACTTGGAATTACTTCTGGCAACAAGTCCTGG
ATCCTGCCTGGCACCTTCTGTTTGATGGGTGCAACCTGACCAGAGAGAGCTGGAAGGCCCTGG
AGCGGGCCAGCTTCTCTAAGCTGAAGCTGCAGCACATCCAGGCCCCACTGTCTGGGAGTTGG
TGCGCCCTCATATCTATGGATATGCTGTGAA**AGT**GTGAGCTGGCAGTTAAGAGCTGAATGG
CTCAAAGAATTTAAAGCTTCAGTTTTACATTTAAATGCTAAGTGGGAGAAGAGAAACCTTTT
TTTTGGGGGGCGGTTTTTTTTGGTTTGTGTTGGTTTTTTTTTTTTTTTTTTGGCAGGAGAATCTC
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTGTACTCTAGCCTGGGTG
ACAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAGAAGTAGAGACAGGGAGAC
GGGGTCTCACTGTGTTGCCTAGGCCGGTCTTGAACTCCTGGGCTCAAGTGATTCTCCACCTT
GACCTCCTAAATTGTTGGGATTACAGGTGTGAGACAGTGCACCTGGCCGAAATAGCTCAAGTT
TCTGAAAAACAAATCTGAATCTATTTGTTATTCTTAGCGTCACTGGTCTGGCTTTCAGAATTA
ACATACAAGGTTGCCACACCTAGTTCTGCCCAGCTTTATGTCTTTTATTCCAGTATTCCACCA
AAGTTTGTTTTCTCTGCATTCCAGTTCTCAAGTCTTAAGATAAAGATTGTACTTGACAGTTTAG
TATATCCATAAACTATTTGAGGTGGTTAAGGTTCTTGGGTTTCATTTTCTTAATACTTTGCT
GAATATTGTAGATTGTAGGCAATGAAAAGTCTACTAAATTAGGAAAACCTTGAATAATTAGG
TATCCTAGGTAAGAGCCCCCTAAACATCAAGCAATCTGTGAGTCTGTAAAGAAATAAATATTTT
TTGGATTATTCTTATCTAATTCACCCCTGTTGGAAGATGATTTCTTTGTTCTTTGCAACTAT
GGAAGCTGTGAAAATCATCACAAGTGCCTCTGAAAGCGAGTGTAGGTTGGTTAGAGGGTTTA
ATATTTTCTGCAATGGTTTGTAGGAATTTTAATAAATGTAGTATATTTTCTGAGATGATTTTG
TAAAGTACTATTTTAAATATCAAATCAACCAATAAATTCACATTTGTGTTAGGAACAAAA

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FIGURE 156

MELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRFTVIYNEQMASKKRELF SNLQ
EFAGPSGKLSLLEVGC GTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVAA
GENMHQVADGSVDVVVCTLVLC SVKNQERILREVC RVL RP GGAFYFMEHVAAECSTWNYFWQQ
VLDPAWHLLFDGCNLTRESWKALERASF SKLKLQHIQAPLSWELVRPHIYGYAVK

Signal peptide:

amino acids 1-29

N-glycosylation site.

amino acids 203-207

N-myristoylation sites.

amino acids 78-84, 80-86, 91-97, 201-207

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FIGURE 157

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT
GCCACGACCGGGCCTCTCCCTGGCGTTTGGTCACCTCTGCTTCATTCTCCACCGCGCCTATGG
TCCCTCTTGGAGCCAGCGTGGCGGGCCTGGCGGCTCCCGGGTGGTGAGAGAGCGGTCCGGGAA
CGATGAAGGCCTCGCAGTGCTGCTGCTGTCTCAGCCACCTCTTGGCTTCCGTCCTCCTCCTGC
TGTTGCTGCCTGAACTAAGCGGGCCCCCTGGCAGTCCTGCTGCAGGCAGCCGAGGCCGCGCCAG
GTCTTGGGCCTCCTGACCCTAGACCACGGACATTACCGCCGCTGCCACCGGGGCCCTACCCCTG
CCCAGCAGCCGGGGCCGTGGTCTGGCTGAAGCTGCGGGGCGCGGGGCTCCGAGGGAGGCAATG
GCAGCAACCCTGTGGCCGGGCTTGAGACGGACGATCACGGAGGGAAGGCCGGGGAAGGCTCGG
TGGGTGGCGGCCTTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA
CCGTGTTGATGGTGGTGAGCGGCGCGGTGCTGGTGTACTTCGTGGTCAGGACGGTCAGGATGA
GAAGAAGAAACCGAAAGACTAGGAGATATGGAGTTTTGGACACTAACATAGAAAATATGGAAT
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTTGATGCCAATCATCCTC
GAAGATAAGAATGTGCCTTTTGATGAAAGAACTTTATCTTTCTACAATGAAGAGTGGAATTTC
TATGTTTAAGGAATAAGAAGCCACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTT
TAACAACCTTTAATTTGCTGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTAT
AGAAGTACTCTATTAATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTG
TTTGAAAATTACTATAAAACGGTGTTTTCTGGTCGGTTTTTGTTCCTGCTTACCATATGATT
GTAAATTGTTTTATGTATTAATCAGTTAATGCTAATTATTTTTGCTGATGTCATATGTTAAAG
AGCTATAAATTCCAACAACCAACTGGTGTGTAAAAATAATTTAAATTTCCCTTTACTGAAAGG
TATTTCCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAT
ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCTCTTAAAAA
AAAAA

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FIGURE 158

MKASQCCCCLSHLLASVLLLLLLLPELSGELAVLLQAAEAAPGLGPPDPRRRTLPELPFGPTPA
QQPGRGLAEAAGPRGSEGGNGSNPVAGLETDDHGGKAGEGSVGGGLAVSPNPGDKPMTQRALT
VLMVVS GAVLVYFVVRTVRMRRNRKTRRYGVLD TN IENMELTPLEQDDEDDNTLFDANHPRR

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 124-140

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,
157-160

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FIGURE 159

GCTGCAGGCGGCGACGGCTACACC**ATG**GGGCCGGCTGCTGCGGGCCGCCCGGCTGCCGCCGCTG
CTTTCGCCCCTGCTGCTTCTGCTGGTTGGGGGAGCGTTCCTGGGTGCCTGTGTGGCTGGGTCT
GATGAGCCTGGCCCAGAGGGCCTCACCTCCACCTCCCTGCTAGACCTCCTGCTGCCCACTGGC
TTGGAGCCACTGGACTCAGAGGAGCCTAGTGAGACCATGGGCCTGGGAGCTGGGCTGGGAGCC
TCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC
TTCTGGGAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTAT
GTTTTTCTGACTTAACTGAGAAGGCAGGTTCCATTGAAGACACTAGCCAGGCTCAAGAGCTG
CCAAACCTCCCCTCTCCCTTGCCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCTCCC
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA
GAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCCAAGCCTCAG
GTCCGTGACTTTTCTCTCACCAGCAGCAGCCAGACCCCAGGGGCCACCAAAAGCAGGCATGAA
GACTCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCCAGCTTGCTG
CTGCCCTCAGTCACCCCAACTACAGTGAATCCGGGGGACCAGGACTCCACCAGCCAAGAGGCA
GAGGCCACAGTGCTGCCAGCTGCAGGGCTTGGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGC
GAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAGCACGAGGAGGTCCCGGCCTTGCT
TCATTCCCTCAAACCACAGCTCCAGTGGGGCCGAGCACCCAGATGAAGATCCCTTGCTCT
AGAACCTCAGCCTCTTCCCCACTGGCCCCTGGAGACATGGAATGACACCTTCCTCTGCTACC
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGG
ATACCCTGGGATTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTAC
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAG
CTCCTGGCCCTGGTGGAAGAGGTGCTGCCCCGCCATGGCAGTGGCCACCATGGGGCCTGGCAC
ATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACACTGGTGGGCGAGCAG
GGGGTGGTGCCCACTCAAGATGTCCTTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAGGAG
ATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGCGGGCCAGCCAGGTGCGCAGC
GACTACGGCACGCTCTTCGTGGTGCTGGTGGTCATTGGGGCCATCTGCATCATCATCATTGCG
CTTGGCCTGCTCTACAACTGCTGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTGCGACGGC
GAGGAGCTGCGCTTCGTGGAGAACGGCTGCCACGACAACCCACGCTGGACGTGGCCAGCGAC
AGCCAGTCGGAGATGCAGGAGAAGCACCCCAGCCTGAACGGCGGGGGGCCCTCAACGGCCCG
GGGAGCTGGGGGGCGCTCATGGGGGGCAAGCGGGACCCCGAGGACTCGGACGTGTTGAGGAG
GACACGCACCTG**TGAG**CGCAGCCGAGGCGCAGGCCGAGTGGGCCGCCAGGACCAAGCGAGGTG
GACCCCGAAACGGACGGCCCGGAGCCCGCACCAGCCCCGCGCTACCCGGGCGCCCCCGCGG
CCTGGCCCTCGGCGCGGGCTCCTTCCCGCTTCCCCGACTTCACACGGCGGGCTTCGGACCAAC
TCCCTCACTCCCGCCCGAGGGGCAGGCCTCAAAGCCCGCCTTGGCCCCGCTTCCCGCCCCTG
AACCCCGGCCCCCGCGGGCGGGCGGGCGGCTTCCTGCGCCCCGGGACTCAATTAAACCGCCC
GGAGACCACGCCGGGGCCCAGCAAAA

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FIGURE 160

MGRLLRAARLPPLLSPLLLLLLVGGAFLGACVAGSDEPGPEGLTSTSLDLLLPTGLEPLDSEE
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPATDYVFPDLTEK
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMPPREEEEEEEEEEREKEEVEKQEEEEEEEL
LPVNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSLLLPSVTPTT
VTPGDQDSTSQEAETVLPAAAGLGVEFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTAP
SGAHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQLLEGQAEEAQSRIPWDSTQV
ICKDWSNLAGKNYIILNMTENIDCEVFRQHRGPQLLALVEEVLP RHGSGHHGAWHISLSKPSE
KEQHLLMTLVGEQGVVPTQDVLSMLGDIRRSLEEIGIQNYSTTSSCQARASQVRSDYGTLFVV
LVVIGAICIIIIALGLLYNCWQRRLPKLKHVSHGEEELRFVENGCHDNPTLDVASDSQSEMQEK
HPSLNGGGALNGPGSWGALMGGKRDPEDSDVFEEDTHL

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 499-521

N-glycosylation sites.

amino acids 106-110, 193-197, 395-399, 480-484

Glycosaminoglycan attachment site.

amino acids 77-81

N-myristoylation sites.amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590**Amidation site.**

amino acids 588-592

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FIGURE 161

CCAGGGCGGAGCGCAGCTGCGCCGGGCTTGGGCGCCTGGGGCCGCGCTCCCCACCGTCGTTT
TCCCCACCGAGGCCGAGGCGTCCCGGAGTC**ATG**GCCGGCCTGAACTGCGGGGTCTCTATCGCA
CTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGCCGCGCGGGGCAGAAGCTTTTGAGATT
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCCGACTCTGCTGGCA
AAACCCTGTTACATCGTCATTTCTAAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAA
AGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAGAATCACTTTGTCATAGAGATCCAGAAA
AATATTGACTGTATGTCAGGCCCATGTCCTTTTGGGGAGGTTCAGCTTCAGCCCTCGACATCG
TTGTTGCCTACCCCTCAACAGAACTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTA
GAGCTGCAGTTTTCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCCAGACGGA
GTCACTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGC
AATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGG
TTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGC
ATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAA
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTCTTCCTGCACACCTGCGGGCCAGC
GTCTCCTTCCTCAACTTCAACCTCTCCAACCTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC
ATCCCGGGCTCCACCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATG
GCGGGGAACCTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCCAGGGATCCTC
CGGCTGCAGTTCCAAGTTTGGTCCAACATCCACAAAATGAAAGCAGTGAG**TGA**AGCCCCACTT
TCCTTTTTCTTCCTCCTCCAGCACCTTCGTTGTTTCCTGGGTAGTCTGCCTGGGTGAGGCTCC
CTTCCTGTTTCTCATCTGTGGCTTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTTCAGG
AAGTGGGTGCTAGGCAGTTAGACAGGCTTGTGGTGAACACCCGGTATGTAGTTCCATTTCA
GCACAATAAAAAGAAATCTGCATTCAAGATGCTAAATTGTTTTTAACGAAAA

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FIGURE 162

MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPTLLAKPCYIVISKR
HITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPSTLNRTFI
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQ
EGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTW
QFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVEFKLEDKQPGNMAGNFNLSLQG
CDQDAQSPGILRLQFQVLVQHPQNESSE

Signal peptide:

amino acids 1-29

N-glycosylation sites.amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,
310-314, 339-343**Tyrosine kinase phosphorylation site.**

amino acids 276-284

N-myristoylation sites.

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309

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FIGURE 163

CAACCACACACCTGGGGAATTGCTGGCCTGACTTCTGACCCCTGACTCCTCATAACCTTCCTC
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCCAGACCCTGGCCCTTCC
CCCGCCCTGTGGTGACTTCATAAAGGTTACTAGCTTCTCCCCTGGCCTTGAGACCCACACGAT
GGCCCTGCTGGCTCTGGCCAGTGCCGTCCCCTCTGCCCTGCTGGCCCTGGCTGTCTTCAGGGT
GCCCCTGCTGGCCTGTCTCCTCTGCTTCACAACCTACTCTGAGCGCCTCCGCATCTGCCAGAT
GTTTGTTGGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCTTCACGGCCGCCTTCCA
GGCCTCTCTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTTGGGGAAG
GTGCAGAGGGAGGGCAGGAGAGGGCCAGAGGGTCAGGCTGAGGGACAGACAGAGAGAAACAGT
CAGAGGAGAAAGGCTCAAAGACCATGAGAACACAGAGACTTAGGGACAGAGAGACACAGACA
GGGAAGACAGCAGGGCAAAGACTCAGAGAGGGGAGGATGGAGAGTCAGAGAGGGGAAGATGG
AGACTCAGAGAGAGGGGAGGATGGAGACTCAGAGAGAGAGGAAGATGGAGACTCAGAGGGAAA
GATGGAGACTCAGGAGTATGGAGAGTCAGAGAGGGGAGGATGGACACTCAGGGGAGGATGGAG
AGTCAGGAGGATGGAGACTCATAGAAAGGGGAGGATGGAGAGTCAGGAGAGGTTGGAGACTGG
AGAGGGAATAGAGACCCAGAAAGGGGAGGATGGAGACTCAGAGGGTGAAGATGGAGACTCAA
AGAGGATGGAACCCAGAGAGAGGAGGACAGAGATGAGGGCAGAGACTAGGGGAAGCAGGATAG
CGACTGGTCGGGGGCAGAGACTCAGGGAGGATAGAGACTCACAGAGAGGTGAGGATAGAGACT
TGGGAGGGACTCAGGAAGCATAGCGACTGTGGGGCAAAGAGTCAGAGAGGGGAGGATACAGAC
TTGGGAGGGCAGAGACTCAGAAACAGAATGTTTCGCATTAGGGACATGGTGTTGCGGGGAGCTG
CCTCCCCCAGCCCCCTGCTCCCTCCCTCACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA
CACCTTCACCCAGATGACCCATGCCCTGCAGGAGCTGGCTGCTGCCCAGGGATCCTTTGAGGT
TGCCTTCCCTGATGCTGCAGAGAAAATGAAGAAGGTCATTACACAGCTTAAAGAAGCCCAGGC
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTCGCCCCGGCGTTTCCTCTGCAGCGGGTGCTACTC
TAGGGTCTGCGACCTCCCGCTGGACTGCCAGTTCAGGATGTGACAGTGACTCGGGGCGACCA
GGCTATGTTTTCTTGCATCGTAACTTCCAGCTGCCAAAGGAGGAGATCACCTATTCCTGGAA
GTTTCGAGGAGGAGGTCTCCGGACTCAGGACTTGTCCTATTTCCGAGATATGCCGCGGGCCGA
AGGATACCTGGCGCGGATCCGGCCGGCTCAGCTCACGCACCGCGGGACGTTCTCCTGCGTGAT
CAAGCAAGACCAGCGCCCCCTGGCCCCGGCTCTACTTCTTTCTTAACGTCCTCGGGGCCCTCGC
ATCAGCGAGTGCGACAGTGTTGGCGTGGTGAGTTCCTGGGGACTCCGGAGCCCCAGCATCTAGC
TCCCCGCTGTCTCAGATCCCACCGAGAAGTCTGGGTTCCCAGCAACCTCCAACCCAGGAGGAT
GTTCTTTTCGATGGTACTGCAGTGGCAACTAACAAAGGTATCTTTCCTCCTTCCCTATCCTATT
TCCATCCTGAAAATAAAGAATATATTTCAACTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAA

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FIGURE 164

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRS PKLEEC EEAFTAAF
QGLSDTEISEETIHTSSVSWGRCRGRAGEAQRVRLRDRQRETVRGERLKD HENNRDLGTERHR
QGKTAGQRLREGRMESQRGEDGDSE RGEDGDSE REEDGDSE GKMETQEYGESERGGWTLRGGW
RVRRMETHRKGRMESQERLETGEG IETQKGEDGDSE GGRWRLKEDGNPERGGQR

Signal peptide:

amino acids 1-26

N-myristoylation site.

amino acids 65-71

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FIGURE 166

MELSDVTLIEGVGNEVMVAGVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH
VDHLVAGQGNPEPTELPHPSEGNDKAEAEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFPGQES
QMKLIYQGRLLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVGS
LMVPVFVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLVFGMYGR

Signal peptide:

amino acids 1-36

Transmembrane domains:

amino acids 246-267, 275-301

N-glycosylation sites.

amino acids 162-166, 211-215

N-myristoylation sites.

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

Cell attachment sequence.

amino acids 97-100

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FIGURE 167

GGCGGCTGTGTGTGCGCGGAGCCGAAGCGCGCAGGCCCGTCCCGGTGGCGCGGGAGCGGGCGGGTGGGGGCGCCA
TGTGGTTCATGTACCTGCTGAGCTGGCTGTGCTCTTCATCCAGGTGGCCTTCATCAGCTGGCTGTGCGGGCTG
GACTCTATTACCTGGCAGAACTGATAGAAGAATACACAGTGGCCACCAGCAGGATCATAAAATACATGATCTGGT
TCTCCACCGCTGTACTGATTGGCCTCTACGTCTTTGAGCGCTTCCCCACCAGCATGATTGGAGTGGGCCTATTCA
CCAACCTCGTCTACTTTGGCCTCCTCCAGACCTCCCCCTTCATCATGCTGACCTCGCCTAACTTCATCCTGTGCT
GTGGACTAGTGGTGGTGAATCATTACCTAGCATTTCAGTTTTTTGCGAGAAGAATATTATCCCCTCTCAGAGGTCC
TGGCCTATTTTCACTTTCTGCTGTGGATAATTCCGTTTGCGTTTTTTGTGTCACTTTTCGGCCGGGAGAACGTCC
TGCCCTCTACCATGCAGCCAGGAGATGATGTCGTCTCCAATTATTTACCAAAGGCAAGCGGGGCAAACGCTTAG
GGATCCTGGTTGTCTTCTCCTTCATCAAAGAGGCCATTCTACCCAGTTCGTGAGAAGATATACTGAACCCCATGCA
GGCAGGATGTGGGGGGCAAGATCAGGAGAGTCAGGCCCTGGGCCTCTATGCCAGGTGGGGACCAGAAGTCGGGA
AGGCACCTTACCACCTGCCCTGGCTTTCTTCCCTCAACTCTGGAGCCCCATCCCCACCCTCCTTGGGGGGCTCAG
CTTGGCTCAGATCTGATGCTTCAAGAGGCTGTAACCTCAGAGGGCACCAGGAGGGTGGCAGAGCCTGCTTAGCC
AGGAGGCCGAGGTCCCTCAGTCCCTCCCTGTCCCTTCCAAGGTGGGTGAGGAGGTTCTGGCCCCGCTGGGGCAGG
CAGGGCAGGGTCTGTGAAGCTTAAGAGCAGATGGTGACAAGTTCTCTGGGCAGGTGGCCATGGGGAGGGGCCATG
GCTTGGCATGTCCAACAGAAATAGTTTTTCTGTTGAACGGTGATTTCTGTCCAAGTGCAGATTTCCGTTTGAAT
AAAGCTTCGCTTCTAGGTGGCACTGTTTGCCCTTAATACCCTGACAGTTTCATCTTCCCTTCTTCCCTGCTAACCTTC
TGCTCTGGACTGGACTCACTTTTCTGCTCCAGGGACTCCTTTTCTGGGTTTGGGTCTTGCCCTTCCCAAGGGACT
GTTCTTGTGGCCCTTAATGGGAAGGGGGCAGGGGTGAGGAGCTGAGCCTGCTCAAGGAGTGGGAAGTGGGGCTAT
AGGCAGCCTCTCTGATGCACCTCTTCCATCTCTTTCCCCAAGGCTCCGTGACTGTCAAAGTGGGAGTAGGAGAG
GGGACAATTTAGGACTGGGCTAGATTTTCAGAAGAACATCTACAATATCCTATTTATAAATCTTCTCTGGGAAA
AGGAGTGGTTTTCTGGCTGAATACTATCTTAGGCTCAAGGAGAAAACAAAATAAAAATTAGCTTCCAGGCAGCCTGT
TTTTAAAGAAATGGGACTAATGGGAGAAGCTGTTTTGTCACTCTAAGAGCATCCAAGCCCTGGCCCGTCTGTGCAC
TCTTGGCTCCTGGGGAGATATATCTGCCTTCTAAGAAGGCAGGCCAGGTCTTGGGCACAGACCTGCATTTGTTGA
CCTTGCACCTCAACTATAGTGCCCTTGCAAGTGCTCAACAGTACATATTGGAATGAAGTCCCTATGAGAGCCATTT
CTGGCCATGTTCTATACCTCAAAGTGAGGCTGGCAGGTACAGAGATGAAGTGTACACATGTGATACATTTAAGCC
ACTGGAAAACCCCTGTGCTTGAAAATATTTCTCTATATCATGCCTGGAGTTCCATCATAGCCCTTCATTTCTCT
TGGCTTTAGCATTTACCTTCTCTTAAGAATACCAGCTTCCCCCTTCCCTGAGAGGAAGAGCACATGTTGGTCTC
CTCTTAGTGTGAACGAGATTGCCAGGCCCTTTTCTCCTATGCACACCAGGATAGACAAGGCAGGGGATACTGGCA
GCCTGCATCATCTCCATTGGGCTGCAGCTGGCCCTACTTTCCCTCCCTCTGCTGCTTGGTCCCTCACCTTGAT
GATGTGGCTTCGCCCCCTCCACTCTACTGCCAGTGTCTCCAGGGGTTGCTAAATCCAGCAGACCCCTTTCTCTG
TCTTACTAGATCTGGGCAGCATTTGACATGGCTGATCACCCCTTGCTTCTTGGATGGCACTTCCCTGGCACCTCT
GTGGCTAGTTGTCTACCTCCCTGGCTGTTCCCTTTCAGGCTTCCGTGCAGGCTTCTCCACTTGCCCATGCACAGT
AGGGTCTTTTCAAGGTTCTGCTGTGGGCTCCCTAGGGGAAGCCCATCCATCTGGATGGTTTCAAGGATGGTGAGGAA
TTTAGAGTTGACCTCCAGCCCCAACATCCTTCTGATCACCTGAACCACAGTTTGTGCTGCCCTCTAGGTGCACAG
ACAATTCAAGTCCATGGCCAGATGGTACTTGCTGTCTTCTGCAAACCTGCCCTTCTGGGTACTTCCCTTGACC
CCGAGATCACTCAGGAGCCAGACAGGAACTTATTCTATTCTGTTTCTCTTTCTGCCCACCACATCCAATCTC
TCAAACGGTCAGGTCTACCTTAACATCTCTTGATTTGAGCCACTCCCACTGTCTATCAGCTTTACCTGGATTAT
CGTGACAGCCTCCTACTGCTTCTCTATCATGTGGCCAGAGCTATCTTCTAAATGCATTGCATAGTTGATCAAG
TCACTCTCTGGCCTAAACCTTCTTGGCTCCCTGCTGCCCTCAGGATAAAGTCTGGACCCCTCAGCATGGCTTG
TGAGACTCATGGTGTCTTGTCCCTGCTCACTCTCTGGTCTCATCACTTGCCCTTCTTGCACTTCTGGTCCCAGC
CTCCTGTATCCAGAGATGCAGTGGCTCTCCATTGCCACTCTGATTCCTCCTTTCTTTTGGTACAGAGAAAGGGT
ACTTTCTCTGTCAAATCTCAACTTAGACTTGACTTCTCCAAGGAGCTTTGGCTATACTCTCTCCTCCCGACCCC
CACCCTGGCATACTACACAGATCACTCTGGGCTCACTTGCCCTGCTAATGGTCATCTCCCAGTAGACTGTAAGC
TCCTTGAGGGCAAGGATTGTGTTGGAATTTTGTATTAAACAGTGCCCTGGCTTGGTGCCTGGCACCTAGAAAGCAC
TCAATAAATGTTTGTTTAATGAA

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FIGURE 168

MWEMYLLSWLSLEFIQVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFESTAVLIGLYVFE
RFPTSMIGVGLFTNLVYFGLLQTFPEIMLTSPNFILSCGLVVVNHYLAFQFFAEYYPFSEVL
AYFTFCLWIIIPFAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGKRGKRLGILVVESFIKEAIL
PSRQKIY

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 126-146

Casein kinase II phosphorylation site.

amino acids 145-148

N-myristoylation sites.

amino acids 73-78, 82-87

Amidation sites.

amino acids 168-171, 171-174

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 91-101

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FIGURE 169

CAAAGCCCTACCCTCACCATTACCCAGGTCCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG
TTAGAAGGTGCAGAGCGTGGAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG
TCCCTGGGCCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCGCGTGAATACA
CATGGCTCTGTTACGAAAAATTAATCAGGTGCTGCTGTTCCCTTCTGATCGTGACCCTCTGTGT
GATTCTGTATAAGAAAGTTCATAAGGGGACTGTGCCCAAGAATGACGCAGATGATGAATCCGA
GACTCCTGAAGAACTGGAAGAAGAGATTCTGTGGTGATTGTGTGCTGCAGCAGGGAGGATGGG
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTTCTATGT
AGTGGGACTCCGGAATACTCTGACTCGAATACGAAAATGGATTGAACATTCCAACTGAGAGA
AATAAACTTTAAAATCGTGGAATTCAACCCGATGGTCCTCAAAGGGAAGATCAGACCAGACTC
ATCGAGGCCTGAATTGCTCCAGCCTCTGAACTTTGTTTCGATTTTATCTCCCTCTACTTATCCA
CCAACACGAGAAAGTCATCTATTTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT
GTATGACACCACCTTGCCCTGGGCCACGCGGCGGCTTTCTCAGATGACTGCGATTTGCCCTC
TGCTCAGGACATAAACAGACTCGTGGGACTTCAGAACACATATATGGGCTATCTGGACTACCG
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCCAGCACCTGCTCTTCAATCCTGGTGTGAT
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAAGCAATTGGAGAAATGGATGCA
AAAGAATGTGGAGGAAAACCTCTATAGCAGCTCCCTGGGAGGAGGGGTGGCCACCTCCCCAAT
GCTGATTGTGTTTCATGGGAAATATTCCACAATTAACCCCTGTGGCACATAAGGCACCTGGG
CTGGAATCCAGATGCCAGATATTCGGAGCATTTTCTGCAGGAAGCTAAATTACTCCACTGGAA
TGGAAGACATAAACCTTGGGACTTCCCTAGTGTTTACAACGACTTATGGGAAAGCTGGTTTGT
TCCTGACCCTGCAGGGATATTTAACTCAATCACCATAGCT**TGA**TATAACTCTACCCTTAAAAT
ATTCCCTGTATAGAAATGTGGAATTGTCCCTTTGTAGCCAACTATAACATTGTTCTTTATGAA
TATTACCTTTGATACATATGATCCACAATATAAAAACCAAAACTACTGTGTGCAAATTATAC
CTTGACCATATAGGCATTGATTAACCTCTTTAAGTACATGTGATAACTATGGAAATCAAGAT
TATGTGACTGAAAAACATAAAGGAAGAGACCCATCTAGATAACAGCAATCAACCTGCTTAATT
CTGAATGACAATTATATCCACAAATTTTAAACTTCTACATGTATTTTTCACATGAAGATCT
CCTTAACAGGTTGCCAACCTTTTCTTTTATAAACTATTACATTTAAAATATGGACGTCTGAA
AAATAAAATATTCATCATTTTTTAAAA

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FIGURE 170

MALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESETPEEELEEEIPVVICAAAGRMG
ATMAAINSISNTDANILFYVVGLRNTLTRIRKWIEHSLREINFKIVEFNPMVLKGKIRPDS
SRPELLQPLNFEVRFYLPLLIHQHEKVIYLDLDDVIVQGGDIQELYDTTLALGHAAAFSDDCDLPS
AQDINRLVGLQNTYMGYLDYRKKAIKDLGISPSTCSFNPGVIVANMTEWKHQRIKQLEKWMQ
KNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFLQEAKLLHWN
GRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 234-238

Tyrosine kinase phosphorylation site.

amino acids 253-261

N-myristoylation sites.amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,
266-272

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FIGURE 171

GCCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAG**ATG**GAGCCCCAGCTGGGGCCTGAGGCTGCC
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGGTCTCAGCCCTGAGCTGTTCTTTCTCC
TTGCCAGCTTCTTCCCTTTCTTCTCTGGTGCCCCAAGTCAGAACCAGCTACAATTTTGGAAGG
ACTTTCCTCGGTCTTGATAAATGCAATGCCTGCATCGGGACATCTATTTGCAAGAAGTTCTTT
AAAGAAGAAATAAGATCTGACAACCTGGCTGGCTTCCCACCTTGGACTGCCTCCCGATTCCCTTG
CTTTCTTATCCTGCAAATTACTCAGATGATTCCAAAATCTGGCGCCCTGTGGAGATCTTTAGA
CTGGTCAGCAAATATCAAAACGAGATCTCAGACAGGAGAATCTGTGCCTCTGCATCAGCCCCA
AAGACCTGCAGCATTGAGCGTGTCTGCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC
AAGCGCCTCACGCCGGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAACTAAAGTTCCTG
TGTATGCTGAGAT**TAA**CACCAGTGAAAAAGCCTGGCATGGAGCCCAGCACTGAGAACTTCCAGA
AAGTGTTAGCCTTCTCCCAACTGTGTTATACCAACCACATTTTCAAATAGTAATCATTAAGA
GGCTTCTGCATCAA

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FIGURE 172

MEPQLGPEAAALRPGWLALLLWVSALSCSFSLPASSLSSLVPQVRTSYNEGRTFLGLDKCNAC
IGTSICKKFFKEEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD
RRICASASAPKTCSEIRVLRKTERFQKWLQAKRLTPDLVQDCHQGORELKFLCMLR

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 100-103

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 158-161

N-myristoylation sites.

amino acids 56-61, 65-70

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 18-28

Prenyl group binding site (CAAX box).

amino acids 179-182

Leucine zipper pattern.

amino acids 5-26

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FIGURE 173

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCCACCTGGGCTGGCTC
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCTGCTCGCTTAAGGCCACTCC
TATTCTACGGCTGACCCCTGGTGGTCACGTGGATCTGTTGCCACGCAAGTCTGGGTCCTTCG
GCGATTGACCGGGGTCCTTGCTGTTCCGGGAGCCTCTCCTAAGCTGCCTGTTCCGCGGAGAGTT
TGGAGGGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCGCAGCACGCTGGAGTCCCG
CTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTCAAGCGGTCGCCGGGACACCCCGTGTGTGG
CAGGCGGCGAAGCGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCCACGGCGGCGGC
CCTGGGAGCAGAGGTGGAGCGACCCCATTAACGCTAAAGATGAAAGGCTGGGGTTGGCTGGCCC
TGCTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG
CATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCA
TTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG
CCCGCTCAGAGGCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG
AATCCAGTGAACCTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCCTCAAGT
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGG
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA
TATCGCATGATGAGCTATGAAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTGAATAATA
TGAAACCAAAAGT

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FIGURE 174

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGsFRINPDGS
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGRNGESSELDLQGIRID
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 12-18, 16-22, 29-35

Endoplasmic reticulum targeting sequence.

amino acids 179-184

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FIGURE 175

CGCAGCGCGGCAGTCCTG**ATG**GGCCCGGCATGGGTTACCGCTGCTGCCCCCTGCTGTCGCTCCTG
GTCGGCGCGCTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAACCTGCAGGGTGGG
AGATTCCCTGATGGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGCG
ACAGTGAAACCCTTTGCCATCGACATATTTCTGTACCAACAAAGATTTTCAGGGATTTTGTC
AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA
GTGGAAAAGGCATTTTGGAGGCAGCCTGCAGGTCCTGGCTCTGGCATCCGAGAGAGACTGGAG
CACCCAGTGTTACACGTGAGCTGGAATGACGCCCGTGCCTACTGTGCTTGGCGGGGAAAACGA
CTGCCACCGGAGGAAGAGTGGGAGTTTGCCGCCCGAGGGGGCTTGAAGGGTCAAGTTTACCCA
TGGGGGAACTGGTTCAGCCAAACCGCACCAACCTGTGGCAGGGAAAGTTCCCCAAGGGAGAC
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCCGCCAGAACAACTAC
GGGCTCTATGACCTCCTGGGGAACGTGTGGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG
CAGGACATGCGCGTCTCTCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC
CGGGCCCCGGGTACCAACCAGGATGGGCAACACTCCAGATTCAGCCTCAGACAACCTCGGTTC
CGCTGTGCTGCAGACGCAGGCCGGCCGAGGGGAGCTG**TAAG**CAGCCGGGTGGTGACAAGGA
GAAAAGCCTTCTAGGGTCACTGTCATTCCCTGGCCATGTTGCAAACAGCGCAATTCCAAGCTC
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC
CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGCCCAATGTGTGTT
GACGATGGCTGGGGGCCAGGTGTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA
CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTAAGCATTTTAAATCTATTC
TCTCCCCCTTTCTCCCTGGATGATTCAGGAAGCTGACATTGTTTCTCAAGGCAGAATTTTCC
TGGTTCTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG
GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAACAGGCAGACATGTAACATTTTA
AAGCACAGTTCAGTCCTAAAAGGGTCTGGGAGAACCAGATGATGTACTAGGTGAAGCATTTGCA
TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT
TTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCTTTCTCTGTTGCCAGGCTAGAGTGCACTG
GTGATCACGGCTCACTCTAGCCTTGAATTCCTGGGCCCCAAGCAATTCTCCACCTCAGCCTCC
TGAGTAGCTGGGACTACAAGTGTGCACCACCATGCCTGGCTAATTTTTTGAATTTTTGTAGTG
ATGGGATCTCGCTCTGTTGCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCCACC
TCGACCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCCCTTCTCCATA
TGCTCCAAAAACATGTCCCTGGAGAGTAGCCTGCTCCACACTGTCACTGGATGTCATGGGG
CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 176

MARHGLPELLLLSLLVGAWLKLGNQATSMVQLQGGRFLMGTNSPDSRDGEGPVREATVKPFA
IDIFPVTNKDFRDFVREKKYRTEAEMFGWSFVFEDEFVSELRNKATQPMKSVLWWLPVEKAFW
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFPAQNNGLYDLLGNVWEWTASPYQAAEQDMRVL
RGASWIDTADGSANHRARVTTRMGNTFDSASDNLGFERCAADAGRPPGEL

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 191-195

N-myristoylation sites.

amino acids 23-29, 25-31, 175-181

Amidation site.

amino acids 159-163

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FIGURE 177

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCCTGCTGGGCCACAGGCGAGCGCTTTAT
TTCTGGAGCTGAGGGCTAAACTTTTTTGACTTTTCTTCTCCTCAACATCTGAATC**ATG**CCAT
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCGTGGTGGCTCAGCTCCTTAACCTTTGGGGCGC
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTTCGCTTCCCGGACAGGAGGCAAGAGCATT
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT
TTTTGTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTGGATGGCT
CAGAGGACTGGGTGTAATAAGAAATTTCTCACGAGGAGAAGGACCTGTTTTTAACTTGACGG
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG
TTAAGATGATGGCTTCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTTCTACAGCAGGGCA
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTTCCAACCTACCAC
ATGGAGACTTTTTCAATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA
TTGTGACTCACATGTCCTCCTGGGTTGAAGAATCTGTTTTGTTCTTTTGG**TAG**TTTTATTAAA
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA
TGACATTCAAATCTCTTCTGTATTCTCTTGCCAGAAAGTGTACATTCTTTTGGCTTGTATAAA
CCCTTTCACCTGTC